



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
- 10 (ii) TITLE OF INVENTION: Bacterial Superantigen
Vaccines
- (iii) NUMBER OF SEQUENCES: 16
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: John Moran
(B) STREET: US Army MPMC -504 Scott Street
MCMR-JA (John Moran-Patent Atty)
(C) CITY: FORT DETRICK
(D) STATE: MARYLAND
(E) COUNTRY: USA
(F) ZIP: 21702-5012
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.5
(D) SOFTWARE: Microsoft Word 6.0
- (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 08/882,431
(B) FILING DATE: June 25, 1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Moran, John
(B) REGISTRATION NUMBER: 26,313
(C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION
45 (A) TELEPHONE: (301) 619-2065
(B) TELEFAX: (301) 619-7714
- (2) INFORMATION FOR SEQUENCE ID NO:1:
- (1) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 830
(B) TYPE: Nucleic Acid

Sub B6

(C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown
 (ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	ATGAAAAAAAA CAGCATTTAC ATTACTTTTA TTCATTGCCC	40
	TAACGTTGAC AACAGTCCA CTTGTAAATG GTAGCGAGAA	80
10	AAGCGAAGAA ATAAATGAAA AAGATTTGCG AAAAAAGTCT	120
	GAATTGCAGG GAACAGCTTT AGGCAATCTT AAACAAATCT	160
	ATTATTACAA TGAAAAAGCT AAAACTGAAA ATAAAGAGAG	200
15	TCACGATCAA TTTCGACAGC ATACTATATT GTTTAAAGGC	240
	TTTTTTTACAG ATCATTCGTG GTATAACGAT TTATTAGTAC	280
20	GTTTGTGATTC AAAGGATATT GTTGATAAAT ATAAAGGGAA	320
	AAAAGTAGAC TTGTATGGTG CTTATGCTGG TTATCAATGT	360
	GCGGGTGGTA CACCAAACAA AACAGCTTGT ATGTATGGTG	400
25	GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA	440
	AAAAGTGCCG ATCAATTTAT GGCTAGACGG TAAACAAAAT	480
30	ACAGTACCTT TGGAAACGGT TAAAACGAAT AAGAAAAATG	520
	TAACTGTTCA GGAGTTGGAT CTTCAAGCAA GACGTTATTT	560
	ACAGGAAAAA TATAATTTAT ATAACCTGA TGTTTTTGAT	600
35	GGGAAGGTTT AGAGGGGATT AATCGTGTTT CATACTTCTA	640
	CAGAACCTTC GGTTAATTAC GATTTATTTG GTGCTCAAGG	680
40	ACAGTATTCA AATACACTAT TAAGAATATA TAGAGATAAT	720
	AAAACGATTA ACTCTGAAAA CATGCATATT GATATATATT	760
	TATATACAAG TTAAACATGG TAGTTTTGAC CAACGTAATG	800
45	TTCAGATTAT TATGAACCGA GAATAATCTA	830

(3) INFORMATION FOR SEQUENCE ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 257
 (B) TYPE: Amino Acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5	Met Lys Lys Thr Ala Phe Thr Leu Leu Leu	1	5	10
10	Phe Ile Ala Leu Thr Leu Thr Thr Ser Pro	15	20	
	Leu Val Asn Gly Ser Glu Lys Ser Glu Glu	25	30	
15	Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser	35	40	
	Glu Lys Gln Gly Thr Ala Leu Gly Asn Leu	45	50	
20	Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala	55	60	
	Lys Thr Glu Asn Lys Glu Ser His Asp Gln	65	70	
25	Phe Arg Gln His Thr Ile Leu Phe Lys Gly	75	80	
30	Phe Phe Thr Asp His Ser Trp Tyr Asn Asp	85	90	
	Leu Leu Val Arg Phe Asp Ser Lys Asp Ile	95	100	
35	Val Asp Lys Tyr Lys Gly Lys Lys Val Asp	105	110	
	Leu Tyr Gly Ala Tyr Ala Gly Tyr Gln Cys	115	120	
40	Ala Gly Gly Thr Phe Asn Lys Thr Ala Cys	125	130	
45	Met Tyr Gly Gly Val Thr Leu His Asp Asn	135	140	
	Asn Arg Leu Thr Glu Glu Lys Lys Val Pro	145	150	
50	Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn			

		155		160
	Thr Val Pro Leu Glu Thr Val Lys Thr Asn			
5		165		170
	Lys Lys Asn Val Thr Val Gln Glu Leu Asp			
		175		180
10	Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys			
		185		190
	Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp			
		195		200
15	Gly Lys Val Gln Arg Gly Leu Ile Val Phe			
		205		210
	His Thr Ser Thr Glu Pro Ser Val Asn Tyr			
20		215		220
	Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser			
		225		230
25	Asn Thr Leu leu Arg Ile Tyr Arg Asp Asn			
		235		240
	Lys Thr Ile asn Ser Glu Asn Met His Ile			
		245		250
30	Asp Ile Tyr Leu Tyr Thr Ser			
		255		

(4) INFORMATION FOR SEQUENCE ID NO:3:

	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 757
	(B) TYPE: Nucleic Acid
	(C) STRANDEDNESS: Unknown
	(D) TOPOLOGY: Unknown
	(ii) Molecule type: DNA
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
	ATGAGAAAAG CGAAGAAATA AATGAAAAAG ATTTGCGAAA 40
	AAAGTCTGAA TTGCAGGGAA CAGCTTTAGG CAATCTTAAA 80
45	CAAATCTATT ATTACAATGA AAAAGCTAAA ACTGAAAATA 120
	AAGAGAGTCA CGATCAATTT CGACAGCATA CTATATTGTT 160
50	TAAAGGCTTT TTTACAGATC ATTCGTGGTA TAACGATTTA 200

TTAGTACGTT TTGATTCAAA GGATATTGTT GATAAATATA 240
 AAGGGAAAAA AGTAGACTTG TATGGTGCTT ATGCTGGTTA 280
 5 TCAATGTGCG GGTGGTACAC CAAACAAAAC AGCTTGTATG 320
 TATGGTGGTG TAACGTTACA TGATAATAAT CGATTGACCG 360
 AAGAGAAAAA AGTGCCGATC AATTTATGGC TAGACGGTAA 400
 10 ACAAATACA GTACCTTTGG AAACGGTTAA AACGAATAAG 440
 AAAAATGTAA CTGTTCAAGG GTTGGATCTT CAAGCAAGAC 480
 15 GTTATTTACA GGAAAAATAT AATTTATATA ACTCTGATGT 520
 TTTTGATGGG AAGGTTCAAG GGGGATTAAT CGTGTTCAT 560
 ACTTCTACAG AACCTTCGGT TAATTACGAT TTATTTGGTG 600
 20 CTCAAGGACA GTATTCAAAT AACTATTAA GAATATATAG 640
 AGATAATAAA ACGATTAACCT CTGAAAACAT GCATATTGAT 680
 25 ATATATTTAT ATACAAGTTA AACATGGTAG TTTTGACCAA 720
 CGTAATGTTC AGATTATTAT GAACCGAGAA TAATCTA 757

(5) INFORMATION FOR SEQUENCE ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:233
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

35 (ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
 5 10
 40 Asp Leu Arg Lys Lys Ser Glu Lys Gln Gly
 15 20
 Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr
 25 30
 45 Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
 35 40
 50 Lys Glu Ser His Asp Gln Phe Arg Gln His
 45 50

	Thr	Ile	Leu	Phe	Lys	Gly	Phe	Phe	Thr	Asp	
					55					60	
5	His	Ser	Trp	Tyr	Asn	Asp	Leu	Leu	Val	Arg	
					65					70	
	Phe	Asp	Ser	Lys	Asp	Ile	Val	Asp	Lys	Tyr	
					75					80	
10	Lys	Gly	Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala	
					85					90	
	Tyr	Ala	Gly	Tyr	Gln	Cys	Ala	Gly	Gly	Thr	
15					95					100	
	Pro	Asn	Lys	Thr	Ala	Cys	Met	Tyr	Gly	Gly	
					105					110	
20	Val	Thr	Leu	His	Asp	Asn	Asn	Arg	Leu	Thr	
					115					120	
	Glu	Glu	Lys	Lys	Val	Pro	Ile	Asn	Leu	Trp	
					125					130	
25	Leu	Asp	Gly	Lys	Gln	Asn	Thr	Val	Pro	Leu	
					135					140	
	Glu	Thr	Val	Lys	Thr	Asn	Lys	Lys	Asn	Val	
30					145					150	
	Thr	Val	Gln	Glu	Leu	Asp	Lys	Gln	Ala	Arg	
					155					160	
35	Arg	Tyr	Leu	Gln	Glu	Lys	Tyr	Asn	Leu	Tyr	
					165					170	
	Asn	Ser	Asp	Val	Phe	Asp	Gly	Lys	Val	Ala	
					175					180	
40	Arg	Gly	Leu	Ile	Val	Phe	His	Thr	Ser	Thr	
					185					190	
	Glu	Pro	Ser	Val	Asn	Tyr	Asp	Leu	Phe	Gly	
45					195					200	
	Ala	Gln	Gly	Gln	Tyr	Ser	Asn	Thr	Leu	Leu	
					205					210	
50	Arg	Ile	Tyr	Arg	Asp	Asn	Lys	Thr	Ile	Asn	
					215					220	

Ser Glu Asn Met His Ile Asp Ile Tyr Leu
 225 230

Tyr Thr Ser

5

(6) INFORMATION FOR SEQUENCE ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15

GAACTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG 40

TTAAAGATGT TTTCGTATAT AAGTTTAGGT GATGTATAGT 80

20

TACTTAATTT TAAAAGCATA ACTTAATTAA TATAAATAAC 120

ATGAGATTAT TAAATATAAT TAAGTTTCTT TTAATGTTTT 160

25

TTTAATTGAA TATTTAAGAT TATAACATAT ATTTAAAGTG 200

TATCTAGATA CTTTTTGGGA ATGTTGGATA AAGGAGATAA 240

AAAATGTATA AGAGATTATT TATTTTCACAT GTAATTTTGA 280

30

TATTCGCACT GATATTAGTT ATTTCTACAC CCAACGTTTT 320

AGCAGAGAGT CAACCAGATC CTAAACCAGA TGAGTTGCAC 360

AAATCGAGTA AATTCAC'TGG TTTGATGGAA GATATGAAAG 400

35

TTTTGTATGA TGATAATCAT GTATCAGCAA TAAACGTTAA 440

ATCTATAGAT CAATTTCTAT ACTTTGACTT AATATATTCT 480

40

ATTAAGGACA CTAAGTTAGG GGATTATGAT AATGTTGAG 520

TCGAATTTAA AAACAAAGAT TTAGCTGATA AATACAAAGA 560

TAAATACGTA GATGTGTTTG GAGCTAATTA TTATTATCAA 600

45

TGTTATTTTT CTAAAAAAC GAATGATATT AATTCGCATC 640

AAACTGACAA ACGAAAAACT TGTATGTATG GTGGTGTAAC 680

50

TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT 720

	ACTGTTTCGGG TATTTGAAGA TGGTAAAAAT TTATTATCTT	760
	TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
5	ATTAGATTAC CTAACCTGTC ACTATTTGGT GAAAAATAAA	840
	AAACTCTATG AATTTAACAA CTCGCCTTAT GAAACGGGAT	880
10	ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
	CATGATGCCT GCACCAGGAG ATAAATTTGC CCAATCTAAA	960
	TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
15	AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
	GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
	AATTAAGGCA GGCACCTTATA GAGTACCTGC CTTTTCTAAT	1120
20	ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
	TAGCATTAAAC CCCTTGTTGC CATTATAGTT TTCACCAACT	1200
25	TTAGCTGAAA TTGGGGGATC ATTTTATCT TTAATATGGA	1240
	TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTCTCTCTT	1280
	TAATTTGTCA GTTAATTTTT TCCATGCATC ATTTGCGTCA	1320
30	AACCTATTTT CATTTGGATT TATTCTTGAC AAATCAATTC	1360
	TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAAAAAT	1400
35	ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
	TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT	1480
	CATTTGCTGT TTTATCGATA ATATTTGCTT CTTTCAAAGC	1520
40	ATCTCTTACA TTTTCCATA AGTCTCTATC TGTTATTTCA	1560
	GAAGCCTTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
45	AAGAATGAAA ACCTGAACCT ACTGTTGTTA AAATAAAGC	1640
	ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCATT	1680
50	TTATTTTCTC CTATAACTTA TTTGCAATCG AT	1712

(7) INFORMATION FOR SEQUENCE ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 265
 (B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10	Met Tyr Lys Arg Leu Phe Ile Ser His Val	5	10
	Ile Leu Ile Phe Ala Leu Ile Leu Val Ile	15	20
15	Ser Thr Pro Asn Val Leu Ala Glu Ser Gln	25	30
	Pro Asp Pro Lys Pro Asp Glu Leu His Lys	35	40
20	Ser Ser Lys Phe Thr Gly Leu Met Glu Asp	45	50
	Met Lys Val Leu Tyr Asp Asp Asn His Val	55	60
25	Ser Ala Ile Asn Val Lys Ser Ile Asp Gln	65	70
	Phe Leu Tyr Phe Asp Leu Ile Tyr Ser Ile	75	80
30	Lys Asp Thr Lys Leu Gly Asp Tyr Asp Asn	85	90
	Val Arg Val Glu Phe Lys Asn Lys Asp Leu	95	100
40	Ala Asp Lys Tyr Lys Asp Lys Tyr Val Asp	105	110
	Val Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys	115	120
45	Tyr Phe Ser Lys Lys Thr Asn Asp Ile Asn	125	130
	Ser His Gln Thr Asp Lys Arg Lys Thr Cys	135	140
50			

	Met Tyr Gly Gly Val Thr Glu His Asn Gly	145	150
5	Asn Gln Leu Asp Lys Tyr Arg Ser Ile Thr	155	160
	Val Arg Val Phe Glu Asp Gly Lys Asn Leu	165	170
10	Leu Ser Phe Asp Val Gln Tyr Asn Lys Lys	175	180
	Lys Val Thr Ala Gln Glu Leu Asp Tyr Leu	185	190
15	Thr Arg His Tyr Leu Val Lys Asn Lys Lys	195	200
	Leu Tyr Glu Phe Asn Asn Ser Pro Tyr Glu	205	210
20	Thr Gly Tyr Ile Lys Phe Ile Glu Asn Gln	215	220
	Asn Phe Trp Tyr Asp Met Met Pro Ala Pro	225	230
25	Gly Asp Lys Phe Ala Gln Ser Lys Tyr Leu	235	240
30	Met Met Tyr Asn Asp Asn Lys Met Val Asp	245	250
	Ser Lys Asp Val Lys Leu Glu Val Tyr Leu	255	260
35	Thr Thr Lys Lys Lys	265	

40 (8) INFORMATION FOR SEQUENCE ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1712
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

50	GAACTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG	40
	TTAAAGATGT TTTCGTATAT AAGTTTAGGT GATGTATAGT	80

	TACTTAATTT	TAAAAGCATA	ACTTAATTAA	TATAAATAAC	120
	ATGAGATTAT	TAAATATAAT	TAAGTTTCCT	TTAATGTTTT	160
5	TTTAATTGAA	TATTTAAGAT	TATAACATAT	ATTTAAAGTG	200
	TATCTAGATA	CTTTTTGGGA	ATGTTGGATA	AAGGAGATAA	240
10	AAAATGTATA	AGAGATTATT	TATTTTACAT	GTAATTTTGA	280
	TATTCGCACT	GATATTAGTT	ATTTCTACAC	CCAACGTTTT	320
	AGCAGAGAGT	CAACCAGATC	CTAAACCAGA	TGAGTTGCAC	360
15	AAATCGAGTA	AATTCACCTG	TTTGATGGAA	AATATGAAAG	400
	TTTTGTATGA	TGATAATCAT	GTATCAGCAA	TAAACGTTAA	440
20	ATCTATAGAT	CAATTTGAT	ACTTTGACTT	AATATATTCT	480
	ATTAAGGACA	CTAAGTTAGG	GAATTATGAT	AATGTTGAG	520
	TCGAATTTAA	AAACAAAGAT	TTAGCTGATA	AATACAAAGA	560
25	TAAATACGTA	GATGTGTTTG	GAGCTAATGC	TTATTATCAA	600
	TGTGCTTTTT	CTAAAAAAC	GAATGATATT	AATTCGCATC	640
30	AAACTGACAA	ACGAAAAACT	TGTATGTATG	GTGGTGTAAC	680
	TGAGCATAAT	GGAAACCAAT	TAGATAAATA	TAGAAGTATT	720
	ACTGTTGCGG	TATTTGAAGA	TGGTAAAAAT	TTATTATCTT	760
35	TTGACGTACA	AACTAATAAG	AAAAAGGTGA	CTGCTCAAGA	800
	ATTAGATTAC	CTAACTCGTC	ACTATTTGGT	GAAAAATAAA	840
40	AAACTCTATG	AATTTAACAA	CTCGCCTTAT	GAAACGGGAT	880
	ATATTAAATT	TATAGAAAAT	GAGAATAGCT	TTTGGTATGA	920
	CATGATGCCT	GCACCAGGAG	ATAAATTTGA	CCAATCTAAA	960
45	TATTTAATGA	TGTACAATGA	CAATAAAATG	GTTGATTCTA	1000
	AAGATGTGAA	GATTGAAGTT	TATCTTACGA	CAAAGAAAAA	1040
50	GTGAAATTAT	ATTTTAGAAA	AGTAAATATG	AAGAGTTAGT	1080
	AATTAAGGCA	GGCACTTATA	GAGTACCTGC	CTTTTCTAAT	1120

5	ATTATTTAGT	TATAGTTATT	TTTGTTATAT	CTCTCTGATT	1160
	TAGCATTAAC	CCCTTGTTGC	CATTATAGTT	TTCACCAACT	1200
	TTAGCTGAAA	TTGGGGGATC	ATTTTTTATCT	TTACTATGGA	1240
	TAGTTACTGT	GTCGCCGTTT	TTAACGATTT	GTTTCTCTTT	1280
10	TAATTTGTCA	GTAAATTTTT	TCCATGCATC	ATTTGCGTCA	1320
	AACCTATTTT	CATTTGGATT	TATTC'TTGAC	AAATCAATTC	1360
15	TTTTAACACT	ATCGGTATTA	ATCGGCTTGT	TATTAAAATT	1400
	ACTAAGTTCA	TCTAAATCAG	CTGTACCCGT	AATACTACTT	1440
	TCGCCACCAT	TATTTAAATT	GTACGTAACA	CCAAC'TGCT	1480
20	CATTTGCTGT	TTTATCGATA	ATATTTGCTT	C'TTTCAAAGC	1520
	ATCTCTTACA	TTTTTCCATA	AGTCTCTATC	TGTTATTTCA	1560
25	GAAGCCTTTG	CAACGT'TATT	AATACCATTA	TAATTTGAAG	1600
	AAGAATGAAA	ACCTGAACCT	ACTGTTGTTA	AAACTAAAGC	1640
	ACTTGCTATC	AATGTTCTTG	TTAATAGTTT	TTTATTCATT	1680
30	TTATTTTCTC	CTATAACTTA	TTTGCAATCG	AT	1712

(9) INFORMATION FOR SEQUENCE ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 265
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Met	Tyr	Lys	Arg	Leu	Phe	Ile	Ser	His	Val
					5					10
45	Ile	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Val	Ile
					15					20
	Ser	Thr	Pro	Asn	Val	Leu	Ala	Glu	Ser	Gln
					25					30
50	Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys

					35					40	
		Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asn
						45					50
5		Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val
						55					60
10		Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln
						65					70
		Phe	Arg	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile
						75					80
15		Lys	Asp	Thr	Lys	Leu	Gly	Asp	Tyr	Asp	Asn
						85					90
		Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu
						95					100
20		Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp
						105					110
		Val	Phe	Gly	Ala	Asn	Ala	Tyr	Tyr	Gln	Cys
						115					120
25		Ala	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn
						125					130
30		Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys
						135					140
		Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly
						145					150
35		Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr
						155					160
		Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu
						165					170
40		Leu	Ser	Phe	Asp	Val	Gln	Tyr	Asn	Lys	Lys
						175					180
45		Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu
						185					190
		Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys
						195					200
50		Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu
						205					210

	Thr Gly Tyr Ile Lys Phe Ile Glu Asn Gln	215	220
5	Asn Phe Trp Tyr Asp Met Met Pro Ala Pro	225	230
	Gly Asp Lys Phe Asp Gln Ser Lys Tyr Leu	235	240
10	Met Met Tyr Asn Asp Asn Lys Met Val Asp	245	250
	Ser Lys Asp Val Lys Leu Glu Val Tyr Leu	255	260
15	Thr Thr Lys Lys Lys	265	

20

(10) INFORMATION FOR SEQUENCE ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1388
	(B) TYPE: Nucleic Acid
25	(C) STRANDEDNESS: Unknown
	(D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30	ATGAGTCAAC CAGATCCTAA ACCAGATGAG TTGCACAAAT	40
	CGAGTAAATT CACTGGTTTG ATGGAAAATA TGAAAGTTTT	80
	GTATGATGAT AATCATGTAT CAGCAATAAA CGTTAAATCT	120
35	ATAGATCAAT TTCGATACTT TGACTTAATA TATTCTATTA	160
	AGGACACTAA GTTAGGGAAT TATGATAATG TTCGAGTCGA	200
40	ATTTAAAAAC AAAGATTTAG CTGATAAATA CAAAGATAAA	240
	TACGTAGATG TGT'TTGAGC TAATGCTTAT TATCAATGTG	280
	CTTTTCTAA AAAAACGAAT GATATTAATT CGCATCAAAC	320
45	TGACAAACGA AAAACTTGTA TGTATGGTGG TGTAAC TGAG	360
	CATAATGGAA ACCAATTAGA TAAATATAGA AGTATTACTG	400
50	TTCGGGTATT TGAAGATGGT AAAAATTTAT TATCTTTTGA	440

	CGTACAAACT AATAAGAAAA AGGTGACTGC TCAAGAATTA	480
	GATTACCTAA CTCGTCAC TA TTTGGTGAAA AATAAAAAAC	520
5	TCTATGAATT TAACAAC TCG CCTTATGAAA CGGGATATAT	560
	TAAATTTATA GAAAATGAGA ATAGCTTTTG GTATGACATG	600
	ATGCCTGCAC CAGGAGATAA ATTTGACCAA TCTAAATATT	640
10	TAATGATGTA CAATGACAAT AAAATGGTTG ATTCTAAAGA	680
	TGTGAAGATT GAAGTTTATC TTACGACAAA GAAAAAGTGA	720
15	AATTATATTT TAGAAAAGTA AATATGAAGA GTTAGTAATT	760
	AAGGCAGGCA CTTATAGAGT ACCTGCCTTT TCTAATATTA	800
	TTTAGTTATA GTTATTTTTG TTATATCTCT CTGATTTAGC	840
20	ATTAACCCCT TGTTGCCATT ATAGTTTTTCAC CAACTTTAG	880
	CTGAAATTGG GGGATCATTT TTATCTTTAC TATGGATAGT	920
25	TACTGTGTCG CCGTTTTTAA CGATTTGTTT CTCTTTTAAT	960
	TTGTCAGTTA ATTTTTTCCA TGCATCATTT GCGTCAAACC	1000
	TATTTCCATT TGGATTTATT CTTGACAAAT CAATTCTTTT	1040
30	AACACTATCG GTATTAATCG GCTTGTTATT AAAATTACTA	1080
	AGTTCATCTA AATCAGCTGT ACCCGTAATA CTACTTTCGC	1120
35	CACCATTATT TAAATTGTAC GTAACACCAA CTGTCTCATT	1160
	TGCTGTTTTA TCGATAATAT TTGCTTCTTT CAAAGCATCT	1200
	CTTACATTTT TCCATAAGTC TCTATCTGTT ATTTCAGAAG	1240
40	CCTTTGCAAC GTTATTAATA CCATTATAAT TTGAAGAAGA	1280
	ATGAAAACCT GAACCTACTG TTGTTAAAAC TAAAGCACTT	1320
45	GCTATCAATG TTCTTGTTAA TAGTTTTTTT TTCATTTTAT	1360
	TTTCTCCTAT AACTTATTTG CAATCGAT	1388

(11) INFORMATION FOR SEQUENCE ID NO:10:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239

(B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Met Ser Gln Pro Asp Pro Lys Pro Asp Glu	
	5	10
10	Leu His Lys Ser Ser Lys Phe Thr Gly Lys	
	15	20
	Met Glu Asn Met Lys Val Leu Tyr Asp Asp	
	25	30
15	Asn His Val Ser Ala Ile Asn Val Lys Ser	
	35	40
	Ile Asp Gln Phe Arg Tyr Phe Asp Leu Ile	
20	45	50
	Tyr Ser Ile Lys Asp Thr Lys Leu Gly Asn	
	55	60
25	Tyr Asp Asn Val Arg Val Glu Phe Lys Asn	
	65	70
	Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys	
	75	80
30	Tyr Val Asp Val Phe Gly Ala Asn Ala Tyr	
	85	90
	Tyr Gln Cys Ala Phe Ser Lys Lys Thr Asn	
35	95	100
	Asp Ile Asn Ser His Gln Thr Asp Lys Arg	
	105	110
40	Lys Thr Cys Met Tyr Gly Gly Val Thr Glu	
	115	120
	His Asn Gly Asn Gln Leu Asp Lys Tyr Arg	
	125	130
45	Ser Ile Thr Val Arg Val Phe Glu Asp Gly	
	135	140
50	Lys Asn Leu Leu Ser Phe Asp Val Gln Thr	
	145	150

	Asn Lys Lys Lys Val Thr Ala Gln Glu Leu	155	160
5	Asp Tyr Leu Thr Arg His Tyr Leu Val Lys	165	170
	Asp Lys Lys Leu Tyr Glu Phe Asn Asn Ser	175	180
10	Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile	185	190
	Glu Asn Glu Asn Ser Phe Trp Tyr Asp Met	195	200
15	Met Pro Ala Pro Gly Asp Lys Phe Asp Gln	205	210
	Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn	215	220
20	Lys Met Val Asp Ser Lys Asp Val Lys Ile	225	230
25	Glu Val Tyr Leu Thr Thr Lys Lys Lys	235	

(12) INFORMATION FOR SEQUENCE ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

35 (ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	TAAGGAGAAT TAAAAATGAA TAAAAAATTA CTAATGAATT	40
40	TTTTTATCGT AAGCCCTTTG TTGCTTGCGA CAACTGCTAC	80
	AGATTTTACC CCTGTTCCCT TATCATCTAA TCAAATAATC	120
45	AAACTGCAA AAGCATCTAC AAACGATAAT ATAAAGGATT	160
	TGCTAGACTG GTATAGTAGT GGGTCTGACA CTTTACAAA	200
	TAGTGAAGTT TTAGATAATT CCAGAGGATC TATGCGTATA	240
50	AAAAACACAG ATGGCAGCAT CAGCTTGATA ATTTTCCGA	280

GTCCTTATTA TAGCCCTGCT TTTACAAAAG GGGAAAAAGT 320
 TGACTTAAAC ACAAAAAGAA CTAAAAAAG CCAACATACT 360
 5 AGCGAAGGAA CTTATATCCA TTTCCAAATA AGTGGCGTTA 400
 CAAATACTGA AAAATTACCT ACTCCAATAG AACTACCTTT 440
 AAAAGTTAAG GTTCATGGTA AAGATAGCCC CTAAAGTAT 480
 10 GGGCCAAAGT TCGATAAAAA ACAATTAGCT ATATCAACTT 520
 TAGACTTTGA AATTCGTCAT CAGCTAACTC AAATACATGG 560
 15 ATTATATCGT TCAAGCGATA AAACGGGTGG TTATTGAAAA 600
 ATAACAATGA ATGACGGATC CACATATCAA AGTGATTTAT 640
 CTAAAAAGTT TGAATACAAT ACTGAAAAAC CACCTATAAA 680
 20 TATTGATGAA ATAAAACTA TAGAAGCAGA AATTAATTAA 720
 TTTACCACTT T 731

25 (13) INFORMATION FOR SEQUENCE ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233
 (B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 30 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35 Met Asn Lys Lys Leu Leu Met Asn Phe Phe
 5 10
 Ile Val Ser Pro Leu Leu Leu Ala Thr Thr
 15 20
 40 Ala Thr Asp Phe Thr Pro Val Pro Leu Ser
 25 30
 Ser Asn Gln Ile Ile Lys Thr Ala Lys Ala
 35 40
 45 Ser Thr Asn Asp Asn Ile Lys Asp Leu Leu
 45 50
 Asp Trp Tyr Ser Ser Gly Ser Asp Thr Phe
 50 55 60

	Thr Asn Ser Glu Val Leu Asp Asn Ser Arg	65	70
5	Gly Ser Met Arg Ile Lys Asn Thr Asp Gly	75	80
	Ser Ile Ser Lys Ile Ile Phe Pro Ser Pro	85	90
10	Tyr Tyr Ser Pro Ala Phe Thr Lys Gly Glu	95	100
	Lys Val Asp Leu Asn Thr Lys Arg Thr Lys	105	110
15	Lys Ser Gln His Thr Ser Gly Thr Tyr Ile	115	120
	His Phe Gln Ile Ser Gly Val Thr Asn Thr	125	130
20	Glu Lys Leu Pro Thr Pro Ile Glu Leu Pro	135	140
	Leu Lys Val Lys Val His Gly Lys Asp Ser	145	150
	Pro Leu Lys Tyr Gly Pro Lys Phe Asp Lys	155	160
30	Lys Gln Leu Ala Ile Ser Thr Leu Asp Phe	165	170
	Glu Ile Arg His Gln Leu Thr Gln Ile His	175	180
35	Gly Leu Tyr Arg Ser Ser Asp Lys Thr Gly	185	190
	Gly Tyr Trp Lys Ile Thr Met Asn Asp Gly	195	200
40	Ser Thr Tyr Gln Ser Asp Leu Ser Lys Lys	205	210
45	Phe Glu Tyr Asn Thr Glu Lys Pro Pro Ile	215	220
	Asn Ile Asp Glu Ile Lys Thr Ile Glu Ala	225	230
50	Glu Ile Asn		

(14) INFORMATION FOR SEQUENCE ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1095
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

	ATCATTAAAT ATAATTAATT TTCTTTTAAAT ATTTT'TTTTAA	40
	TTGAATATTT AAGATTATAA GATATATTTA AAGTGTATCT	80
15	AGATACTTTT TGGGAATGTT GGATGAAGGA GATAAAAAATG	120
	AATAAGAGTC GATTTATTTT ATGCGTAATT TTGATATTCG	160
20	CACTTATACT AGTTCTTTTT ACACCCAACG TATTAGCAGA	200
	GAGCCAACCA GACCCTACGC CAGATGAGTT GCACAAAGCG	240
	AGTAAATTCA CTGGTTTGAT GGAAAATATG AAAGTTTAT	280
25	ATGATGATCA TTATGTATCA GCAACTAAAG TTAAGTCTGT	320
	AGATAAATTT AGGGCACATG ATTTAATTTA TAACATTAGT	360
30	GATAAAAAAC TGAAAAATTA TGACAAAGTG AAAACAGAGT	400
	TATTAAATGA AGGTTTAGCA AAGAAGTACA AAGATGAAGT	440
	AGTTGATGTG TATGGATCAA ATTACTATGT AAAGTGCTAT	480
35	TTTTCATCCA AAGATAATGT AGGTAAAGTT ACAGGTGGCA	520
	AAACTTGTAT GTATGGAGGA ATAACAAAAC ATGAAGGAAA	560
40	CCACTTTGAT AATGGGAACT TACAAAATGT ACTTATAAGA	600
	GTTTATGAAA ATAAAAGAAA CACAATTTCT TTTGAAGTGC	640
	AAACTGATAA GAAAAGTGTA ACAGCTCAAG AACTAGACAT	680
45	AAAAGCTAGG AATTTT'TTAA TTAATAAAAA AAATTTGTAT	720
	GAGTTTAACA GTTCACCATA TGAAACAGGA TATATAAAAT	760
50	TTATTGAAAA TAACGGCAAT ACTTTT'TGGT ATGATATGAT	800

	GCCTGCACCA GCGATAAGT TTGACCAATC TAAATATTTA	840
	ATGATGTACA ACGACAATAA AACGGTTGAT TCTAAAAGTG	880
5	TGAAGATAGA AGTCCACCTT ACAACAAAGA ATGGATAATG	920
	TTAATCCGAT TTTGATATAA AAAGTGAAAG TATTAGATAT	960
	ATTTGAAAGG TAAGTACTTC GGTGCTTGCC TTTTtaggAT	1000
10	GCATATATAT AGATTAAACC GCACTTCTAT ATTAATAGAA	1040
	AGTGCGGTTA TTTATACACT CAATCTAAAC TATAATAATT	1080
15	GGAATCATCT TCAA	1095

(15) INFORMATION FOR SEQUENCE ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 266
20	(B) TYPE: Amino Acid
	(C) STRANDEDNESS: Unknown
	(D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25	Met Asn Lys Ser Arg Phe Ile Ser Cys Val	5	10
30	Ile Leu Ile Phe Ala Leu Ile Leu Val Leu	15	20
	Phe Thr Pro Asn Val Leu Ala Glu Ser Gln	25	30
35	Pro Asp Pro Thr Pro Asp Glu Leu His Lys	35	40
40	Ala Ser Lys Phe Thr Gly Leu Met Glu Asn	45	50
	Met Lys Val Leu Tyr Asp Asp His Tyr Val	55	60
45	Ser Ala Thr Lys Val Lys Ser Val Asp Lys	65	70
	Phe Arg Ala His Asp Leu Ile Tyr Asn Ile	75	80
50	Ser Asp Lys Lys Leu Lys Asn Tyr Asp Lys		

					85					90
	Val	Lys	Thr	Glu	Leu 95	Leu	Asn	Glu	Gly	Leu 100
5										
	Ala	Lys	Lys	Tyr	Lys 105	Asp	Glu	Val	Val	Asp 110
10	Val	Tyr	Gly	Ser	Asn 115	Tyr	Tyr	Val	Asn	Cys 120
	Tyr	Phe	Ser	Ser	Lys 125	Asp	Asn	Val	Gly	Lys 130
15	Val	Thr	Gly	Gly	Lys 135	Thr	Cys	Met	Tyr	Gly 140
	Gly	Ile	Thr	Lys	His 145	Glu	Gly	Asn	His	Phe 150
20										
	Asp	Asn	Gly	Asn	Leu 155	Gln	Asn	Val	Leu	Ile 160
25	Arg	Val	Tyr	Glu	Asn 165	Lys	Arg	Asn	Thr	Ile 170
	Ser	Phe	Glu	Val	Gln 175	Thr	Asp	Lys	Lys	Ser 180
30	Val	Thr	Ala	Gln	Glu 185	Leu	Asp	Ile	Lys	Ala 190
	Arg	Asn	Phe	Leu	Ile 195	Asn	Lys	Lys	Asn	Leu 200
35										
	Tyr	Glu	Phe	Asn	Ser 205	Ser	Phe	Tyr	Glu	Thr 210
40	Gly	Tyr	Ile	Lys	Phe 215	Ile	Glu	Asn	Asn	Gly 220
	Asn	Thr	Phe	Trp	Tyr 225	Asp	Met	Met	pro	Ala 230
45	Pro	Gly	Asp	Lys	Phe 235	Asp	Gln	Ser	Lys	Tyr 240
	Leu	Met	Met	Tyr	Asn 245	Asp	Asn	Lys	Thr	Val 250
50										
	Asp	Ser	Lys	Ser	Val 255	Lys	Ile	Glu	Val	His 260

Leu Thr Thr Lys Asn Gly
265

5 (16) INFORMATION FOR SEQUENCE ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Unknown
10 (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

15	TCATGTTTGA CAGCTTATCA TCGATAAGCT TACTTTTTCGA	40
	ATCAGGTCTA TCCTTGAAAC AGGTGCAACA TAGATTAGGG	80
	CATGGAGATT TACCAGACAA CTATGAACGT ATATACTCAC	120
20	ATCACGCAAT CGGCAATTGA TGACATTGGA ACTAAATTCA	160
	ATCAATTTGT TACTAACAAG CAACTAGATT GACAACTAAT	200
	TCTCAACAAA CGTTAATTTA ACAACATTCA AGTAACTCCC	240
25	ACCAGCTCCA TCAATGCTTA CCGTAAGTAA TCATAACTTA	280
	CTAAACCTT GTTACATCAA GGTTTTTTCT TTTTGTCTTG	320
30	TTCATGAGTT ACCATAACTT TCTATATTAT TGACAACTAA	360
	ATTGACAACT CTTCAATTAT TTTTCTGTCT ACTCAAAGTT	400
	TTCTTCATTT GATATAGTCT AATTCCACCA TCACTTCTTC	440
35	CACTCTCTCT ACCGTCACAA CTTCATCATC TCTCACTTTT	480
	TCGTGTGGTA ACACATAATC AAATATCTTT CCGTTTTTAC	520
40	GCACTATCGC TACTGTGTCA CCTAAAATAT ACCCCTTATC	560
	AATCGCTTCT TTAAACTCAT CTATATATAA CATATTTTAT	600
	CCTCCTACCT ATCTATTCGT AAAAAGATAA AAATAACTAT	640
45	TGTTTTTTTT GTTATTTTAT AATAAAATTA TTAATATAAG	680
	TTAATGTTTT TTAAAAATAT ACAATTTTAT TCTATTTATA	720
50	GTTAGCTATT TTTTCATTGT TAGTAATATT GGTGAATTGT	760

	AATAACCTTT	TTAAATCTAG	AGGAGAACCC	AGATATAAAA	800
	TGGAGGAATA	TTAATGGAAA	ACAATAAAAA	AGTATTGAAG	840
5	AAAATGGTAT	TTTTTGTTTT	AGTGACATTT	CTTGGAATAA	880
	CAATCTCGCA	AGAGGTATTT	GCTCAACAAG	ACCCCGATCC	920
10	AAGCCAACTT	CACAGATCTA	GTTTAGTTAA	AAACCTTCAA	960
	AATATATATT	TTCTTTATGA	GGGTGACCCT	GTTACTCACG	1000
	AGAATGTGAA	ATCTGTTGAT	CAACTTAGAT	CTCACGATTT	1040
15	AATATATAAT	GTTTCAGGGC	CAAATTATGA	TAAATTAAAA	1080
	ACTGAACTTA	AGAACCAAGA	GATGGCAACT	TTATTTAAGG	1120
20	ATAAAAACGT	TGATATTTAT	GGTGTAGAAT	ATTACCATCT	1160
	CTGTTATTTA	TGTGAAAATG	CAGAAAGGAG	TGCATGTATC	1200
	TACGGAGGGG	TAACAAATCA	TGAAGGGAAT	CATTTAGAAA	1240
25	TTCCTAAAAA	GATAGTCGTT	AAAGTATCAA	TCGATGGTAT	1280
	CCAAAGCCTA	TCATTTGATA	TTGAAACAAA	TAAAAAAATG	1320
30	GTAAC TGCTC	AAGAATTAGA	CTATAAAGTT	AGAAAATATC	1360
	TTACAGATAA	TAAGCAACTA	TATACTAATG	GACCTTCTAA	1400
	ATATGAAACT	GGATATATAA	AGTTCATACC	TAAGAATAAA	1440
35	GAAAGTTTTT	GGTTTGATTT	TTTCCCTGAA	CCAGAATTTA	1480
	CTCAATCTAA	ATATCTTATG	ATATATAAAG	ATAATGAAAC	1520
40	GCTTGACTCA	AACACAAGCC	AAATTGAAGT	CTACCTAACA	1560
	ACCAAGTAAC	TTTTTGCTTT	TGGCAACCTT	ACCTACTGCT	1600
	GGATTTAGAA	ATTTTATTGC	AATTCTTTTA	TTAATGTAAA	1640
45	AACCGCTCAT	TTGATGAGCG	GTTTTGTCTT	ATCTAAAGGA	1680
	GCTTTACCTC	CTAATGCTGC	AAAATTTTAA	ATGTTGGATT	1720
50	TTTGTATTTG	TCTATTGTAT	TTGATGGGTA	ATCCCATTTT	1760
	TCGACAGACA	TCGTCGTGCC	ACCTCTAACA	CCAAAATCAT	1800

AGACAGGAGC TTGTAGCTTA GCAACTATTT TATCGTC

1837

(17) INFORMATION FOR SEQUENCE ID NO:16:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251

(B) TYPE: Amino Acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

10

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	Met	Glu	Asn	Asn	Lys	Lys	Val	Leu	Lys	Lys	
					5					10	
15	Met	Val	Phe	Phe	Val	Leu	Val	thr	Phe	Leu	
					15					20	
20	Gly	Leu	Thr	Ile	Ser	Gln	Glu	Val	Phe	Ala	
					25					30	
	Gln	Gln	Asp	Pro	Asp	Pro	Ser	Gln	Leu	His	
					35					40	
25	Arg	Ser	Ser	Leu	Val	Lys	Asn	Leu	Gln	Asn	
					45					50	
	Ile	Tyr	Phe	Leu	Tyr	Glu	Gly	Asp	Pro	Val	
					55					60	
30	Thr	His	Glu	Asn	Val	Lys	Ser	Val	Asp	Gln	
					65					70	
	Leu	Arg	Ser	His	Asp	Leu	Ile	Tyr	Asn	Val	
35					75					80	
	Ser	Gly	Pro	Asn	Tyr	Asp	Lys	Leu	Lys	Thr	
					85					90	
40	Glu	Leu	Lys	Asn	Gln	Glu	Met	Ala	Thr	Leu	
					95					100	
	Phe	Lys	Asp	Lys	Asn	Val	Asp	Ile	Tyr	Gly	
					105					110	
45	Val	Glu	Tyr	Tyr	His	Leu	Cys	Tyr	Leu	Cys	
					115					120	
	Glu	Asn	Ala	Glu	Arg	Ser	Ala	Cys	Ile	Tyr	
50					125					130	

	Gly Gly Val Thr Asn His Glu Gly Asn His	135	140
5	Leu Glu Ile Pro Lys Lys Ile Val Val Lys	145	150
	Val Ser Ile Asp Gly Ile Gln Ser Leu Ser	155	160
10	Phe Asp Ile Glu Thr Asn Lys Lys Met Val	165	170
	Thr Ala Gln Glu Leu Asp Tyr Lys Val Arg	175	180
15	Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr	185	190
	Thr Asn Gly Pro Ser Lys Tyr Glu Thr Gly	195	200
	Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu	205	210
25	Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro	215	220
	Glu Phe Thr Gln Ser Lys Tyr Leu Met Ile	225	230
30	Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn	235	240
	Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr	245	250
	Lys		

40

45